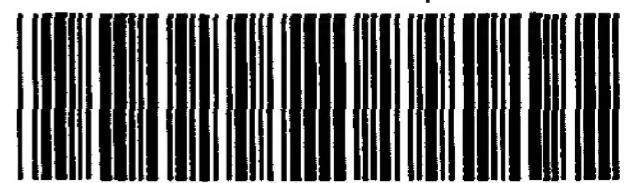


3590
0429

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,106B

DATE: 05/02/2002
TIME: 17:04:59

Input Set : A:\10621021004 sub seq.txt
Output Set: N:\CRF3\05022002\I873106B.raw

4 <110> APPLICANT: Reinherz, Ellis L.
 5 Freund, Christian
 6 Li, Jing
 7 Nishizawa, Kazuhisa
 8 Wagner, Gerhard
 10 <120> TITLE OF INVENTION: Cloning and Characterization of a CD2
 11 Binding Protein (CD2BP2)
 14 <130> FILE REFERENCE: 1062.1021-004
 16 <140> CURRENT APPLICATION NUMBER: US 09/873,106B
 17 <141> CURRENT FILING DATE: 2001-06-01
 19 <150> PRIOR APPLICATION NUMBER: US 60/111,007
 20 <151> PRIOR FILING DATE: 1998-12-04
 22 <150> PRIOR APPLICATION NUMBER: US 60/115,647
 23 <151> PRIOR FILING DATE: 1999-01-13
 25 <150> PRIOR APPLICATION NUMBER: PCT/US99/26993
 26 <151> PRIOR FILING DATE: 1999-11-15
 28 <160> NUMBER OF SEQ ID NOS: 25
 30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1299
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (121)...(1143)
 41 <400> SEQUENCE: 1
 42 agtcctcttc cgggtgatgg cggcgggtgc cccggatgta gccctggcgc aagcatctct 60
 43 tctttttcc acctcgccctt ccgcggattc ccagcttgag aaacacacctt ttgccccgtc 120
 44 atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168
 45 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
 46 1 5 10 15
 48 gag gat gaa atc att gtc ccc aag aag ctg gtg gac cct gtg gct 216
 49 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
 50 20 25 30
 52 ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
 53 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
 54 35 40 45
 56 agc gat gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312
 57 Ser Asp Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
 58 50 55 60
 60 atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360
 61 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
 62 65 70 75 80

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Input Set : A:\10621021004 sub seq.txt
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64	agc gag ggg ggt	cggt	atc aca ccc ttt	aac ctg cag gag gag	atg	408
65	Ser Glu Gly Gly	Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met				
66	85	90	95			
68	gag gaa ggc cac	ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat				456
69	Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp					
70	100	105	110			
72	gct cag atc cga gac agc	tgg ctg gac aac att gac tgg gtg aag atc				504
73	Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile					
74	115	120	125			
76	cgg gag cgg cca cct	ggc cag cgc cag gcc tca gac tcg gag gag gag				552
77	Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu					
78	130	135	140			
80	gac agc ttg ggc cag acc tca atg agt	gcc caa gcc ctc ttg gag gga				600
81	Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly					
82	145	150	155	160		
84	ctt ttg gag ctc cta ttg cct aga gag aca	gtg gct ggg gca ctg agg				648
85	Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg					
86	165	170	175			
88	cgt ctg ggg gcc cga gga ggc aaa	ggg aga aag ggg cct ggg caa				696
89	Arg Leu Gly Ala Arg Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln					
90	180	185	190			
92	ccc agt tcc cct cag cgc ctg gac	cggt ctc tcc ggg ttg gcc gac cag				744
93	Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln					
94	195	200	205			
96	atg gtg gcc cgg ggc aac ctt	ggt gtg tac cag gaa aca agg gaa cgg				792
97	Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg					
98	210	215	220			
100	ttg gct atg cgt ctg aag ggt	ttg ggg tgt cag acc cta gga ccc cac				840
101	Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His					
102	225	230	235	240		
104	aat ccc aca ccc cca ccc tcc	ctg gac atg ttc gct gag gag ttg gcg				888
105	Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala					
106	245	250	255			
108	gag gag gaa ctg gag acc cca acc cct acc cag aga gga gaa gca gag					936
109	Glu Glu Glu Leu Glu Thr Pro Thr Pro Gln Arg Gly Glu Ala Glu					
110	260	265	270			
112	tcg cgg gga gat ggt ctg gtg gat gtg atg tgg gaa tat aag tgg gag					984
113	Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu					
114	275	280	285			
116	aac acg ggg gat gcc gag ctg tat ggg ccc ttc acc agc gcc cag atg					1032
117	Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met					
118	290	295	300			
120	cag acc tgg gtg agt gaa ggc tac ttc ccg gac ggt gtt tat tgc cgg					1080
121	Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg					
122	305	310	315	320		
124	aag ctg gac ccc cct ggt ggt cag ttc tac aac tcc aaa cgc att gac					1128
125	Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp					
126	325	330	335			
128	ttt gac ctc tac acc tgagcctgct	ggggggcccaag ttttgtggc ctttcttcc				1183

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Input Set : A:\10621021004 sub seq.txt
Output Set: N:\CRF3\05022002\I873106B.raw

129 Phe Asp Leu Tyr Thr
130 340
132 tggactttgt ggaggaggca ccaagtgtct caggcagcga gaaaaatttga ggccatTTT 1243
133 cagtcaattt cccttcccataaaaagcct tagttgtgta aaaaaaaaaaaa aaaaaaa 1299
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 341
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 2
141 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Asp
142 1 5 10 15
143 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
144 20 25 30
145 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
146 35 40 45
147 Ser Asp Glu Glu Glu Asp Asp Asp Gly Ser Ser Lys Tyr Asp
148 50 55 60
149 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
150 65 70 75 80
151 Ser Glu Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
152 85 90 95
153 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
154 100 105 110
155 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
156 115 120 125
157 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
158 130 135 140
159 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
160 145 150 155 160
161 Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
162 165 170 175
163 Arg Leu Gly Ala Arg Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
164 180 185 190
165 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
166 195 200 205
167 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
168 210 215 220
169 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
170 225 230 235 240
171 Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
172 245 250 255
173 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
174 260 265 270
175 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
176 275 280 285
177 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
178 290 295 300
179 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
180 305 310 315 320

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Input Set : A:\10621021004 sub seq.txt
Output Set: N:\CRF3\05022002\I873106B.raw

181 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
182 325 330 335
183 Phe Asp Leu Tyr Thr
184 340
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 26
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
192 <400> SEQUENCE: 3
193 Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr
194 1 5 10 15
195 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly
196 20 25
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 27
201 <212> TYPE: PRT
202 <213> ORGANISM: Caenorhabditis elegans
204 <400> SEQUENCE: 4
205 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu
206 1 5 10 15
207 Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly
208 20 25
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 27
213 <212> TYPE: PRT
214 <213> ORGANISM: Caenorhabditis elegans
216 <400> SEQUENCE: 5
217 Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn
218 1 5 10 15
219 Val Trp Phe Lys Ala Gly Tyr Phe Thr Asp Glu
220 20 25
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 27
225 <212> TYPE: PRT
226 <213> ORGANISM: Caenorhabditis elegans
228 <400> SEQUENCE: 6
229 Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu
230 1 5 10 15
231 Asp Trp Tyr Gln Lys Gly Tyr Phe Ser Asp Asn
232 20 25
235 <210> SEQ ID NO: 7
236 <211> LENGTH: 29
237 <212> TYPE: PRT
238 <213> ORGANISM: Saccharomyces cerevisiae
240 <400> SEQUENCE: 7
241 Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser
242 1 5 10 15
243 Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr
244 20 25

RAW SEQUENCE LISTING

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Input Set : A:\10621021004 sub seq.txt
Output Set: N:\CRF3\05022002\I873106B.raw

247 <210> SEQ ID NO: 8
248 <211> LENGTH: 27
249 <212> TYPE: PRT
250 <213> ORGANISM: Saccharomyces cerevisiae
252 <400> SEQUENCE: 8
253 Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser
254 1 5 10 15
255 Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr
256 20 25
259 <210> SEQ ID NO: 9
260 <211> LENGTH: 17
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Motif in CD2 binding region of CD2BP2
W--> 268 <221> NAME/KEY: VARIANT
269 <222> LOCATION: 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 14
270 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W-> 272 <400> 9
W-> 273 Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Thr
274 1 5 10 15
275 Phe
279 <210> SEQ ID NO: 10
280 <211> LENGTH: 6
281 <212> TYPE: PRT
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: CD2BP2 binding region
288 <400> SEQUENCE: 10
289 Pro Pro Pro Gly His Arg
290 1 5
293 <210> SEQ ID NO: 11
294 <211> LENGTH: 70
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapiens
298 <400> SEQUENCE: 11
299 Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro
300 1 5 10 15
301 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro
302 20 25 30
303 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
304 35 40 45
305 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser
306 50 55 60
307 Leu Ser Pro Ser Ser Asn
308 65 70
311 <210> SEQ ID NO: 12
312 <211> LENGTH: 8
313 <212> TYPE: DNA